

IntelliGenetics

**FastDB - Fast Pairwise Comparison of Sequences
Release 5.4**

Results file seq8-seq18-232-723.res made by tport on Thu 27 Oct 105 16:23:23-PST.

Query sequence being compared: US-10-756-778-8 (1-492)
 Number of sequences searched: 1
 Number of scores above cutoff: 1

Results of the initial comparison of US-10-756-778-8 (1-492) with:
File : rooke778.pep

	100-	50-	0
N			
U			
M			
B			
B			
E			
R			
O			
P			
S			
E			
Q			
U			
E			
N			
C			
E			
S			
SCORE	54	107	161
STDEV	0	215	268
	322	376	429
	483		

Sequence Name	Description	Length	Score	Init. Opt.
1. SEQ18-232-723	Sequence 18, Application US/	492	483	0.00 0

1. US-10-7560778-0 (1-492)
SE018-2325723 Sequence 18, Application US/10756778

```
Initial Score      = 483  Optimized Score = 484  Significance = 0.00
Residue Identity = 96%  Matches      = 477  Mismatches = 14
Gaps              = 0    Conservative Substitutions = 1
```

X 10 20 30 40 50 60 70
 I A B P S T V I T Q P I L N D N P I K Y I A K L F S T N Q S D L O Y P V L T I P L R A Q C V M H L L K D A T T S V M G Q I D S Q
 M A E P S T V I T Q P I L N D N P I K Y I A K L F S T N Q S D L O Y P V L T I P L R A Q C V M H L L K D A T T S V M G Q I D S Q
 X 10 20 30 40 50 60 70

QLNGYKAEILRLIKVYTNQDVTNTYNOGLELEKAKPLNTSDPEYLOAGRPDISVLRSNFKSVKMKWNVKAKYK
QLNGYKAEILRLIKVYTNQDVTNTYNOGLELEKAKPLNTSDPEYLOAGRPDISVLRSNFKSVKMKWNVKAKYK
QLNGYKAEILRLIKVYTNQDVTNTYNOGLELEKAKPLNTSDPEYLOAGRPDISVLRSNFKSVKMKWNVKAKYK

RGMAASLSLAALPFTGPNYPKQALKVQSRQIPAPVIGIGITISQDSGPTFGSMGFVKTTDQIDALLRQ
RGMAASLSLAALPFTGPNYPKQALKVQSRQIPAPVIGITISQDSHGTFGSMGFVKTTDQIDALLR
RGMAASLSLAALPFTGPNYPKQALKVQSRQIPAPVIGITISQDSHGTFGSMGFVKTTDQIDALLR

220 230 240 250 260 270 280
LMELYIQPGAYFWIVESDWKVRATYNDYIGKGGSTGAAHMHSSDPSAIYTSALGAGCAYAPNTVGVR
LMELYIQPGAYFWIVESDWKVRATYNDYIGKGGSTGAAHMHSSDPSAIYTSALGAGCAYAPNTVGVR
LMELYIQPGAYFWIVESDWKVRATYNDYIGKGGSTGAAHMHSSDPSAIYTSALGAGCAYAPNTVGVR

SHGSGSYTKGMAPANTNAYAPPEPKYGYKLSHSVAYSGLSKAPDADSVNFGFRPVLLNEANQLLTOTALQI 300 310 320 330 340 350 360

SHGSGSYTKGMAPANTNAYAPPEPKYGYKLSHSVAYSGLSKAPDADSVNFGFRPVLLNEANQLLTOTALQI 300 310 320 330 340 350 360

PBAGITDVPAPGRTPEEPINGQDAIRIWESFTSGFGTIVDSPOQKIKIYRIANLNSASTVSYTYNQ
PAGITGVDPAPGRTPEEPINGQDAIIWESFTSGFGTIVDSPOQKIKIYRIANLNSASTVSYTYNQ

440 450 460 470 480 490 X
TFPTDILNTSLDPNGVRNGSYTLVEGPPIBFSQGTNIPKLGSGKEPAIDSIIPSPV
TFPTDILNTSLDPNGVRNGSYTLVEGPPIBFSQGTNIPKLGSGKEPAIDSIIPSPV
TFPTDILNTSLDPNGVRNGSYTLVEGPPIBFSQGTNIPKLGSGKEPAIDSIIPSPV
TFPTDILNTSLDPNGVRNGSYTLVEGPPIBFSQGTNIPKLGSGKEPAIDSIIPSPV
440 450 460 470 480 490 X